

**Amendments to the claims:**

Please amend the claims as shown below.

1. (Currently Amended) A composition comprising a substantially purified Avilll peptide with cellulase activity and, said Avilll peptide comprising a catalytic domain of a glycosyl hydrolase family 74 (GH74\_Ace) enzyme having at least 70 90% identity to SEQ ID NO. 1, said Avilll peptide comprising a catalytic domain of a glycosyl hydrolase family 74 (GH74\_Ace) enzyme and a carbohydrate binding domain (CBD) III., the catalytic domain GH74\_Ace having a sequence identical to SEQ ID NO. 3 in each conserved position marked by an asterisk (\*), as shown below in comparison to *Aspergillus aculeatus* Avicelase III (Avilll\_Aac):

GH74_Ace	AVTPOVTVWSNVIACCCCFVTDCTIVPNECAPCILVPTDICCIVYRWDAANCRWIPPLIDWVG
Avilll_Aac	AASQVYTNKNTVTCGGCGPTTCIVTPDIAKCVAVARTDICCIVRLNSDDTWTPLMDWVG
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GH74_Ace	WNTHQHGVGIVGIAADPDTNPNWVWVAVCMVNTNSHDNDGATLRCSDOCATWQITPLAFKLG
Avilll_Aac	NDTHIDWGTIDALATDNDV2DRWVAVCMVNTNSHDNDGATLRCSDOCATWQITPLAFKLG
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GH74_Ace	CNMPGRCGMGERLAVDPNKNVILYFGCAPGGKGLWRSTDSCATWQMTNFDPDVCTYIANPTD
Avilll_Aac	CNMPGRCGMGERLAVDPNKNVILYFGCAPGGKGLWRSTDSCATWQMTNFDPDVCTYFQ9582
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GH74_Ace	TTCYQSDIQGVIAVVAFDKSESSSLQQLKXTIFVGVADPNNPVFWSDCCATWQAVPGAP-T
Avilll_Aac	TYTSBPDVGIAMVTFDGTSESSCGATPRIFVGVADACKGVFKSEDAGATWAVVSGEPQY
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GH74_Ace	GTFPQHNGPQDVAHIVLWATGNTCCPUDG88CDWVWQGVTACTWTRISAVPSTDANDP
Avilll_Aac	GFLPKHKGVLSPPEKTLTYTSYANGACPYDGTNCTVWVYNTSCVNTDIP-TSLASTPP
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GH74_Ace	GYGGLTIDRQRPNTIVATQGWWPDTTIFRSTDGGATWTRIWBTGPNRQLRIVLQIC
Avilll_Aac	GYGGLSVDLQVPTLWVIAALNCWNPDLIFRSTDGGATWSPVWVWNGYPSINTTIVSVDIC
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GH74_Ace	AEPWVTVGVQNTIVTSPKLQWMDAMADPPNDRMLYCTGATLYATNDPLTKWDSCCGI
Avilll_Aac	NAPWIQDTSTDQFP-VRVQWNVELAIDPPDSNWLYVCTGCLTVYCCNDLTNWDSKRW
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GH74_Ace	IIAPNWKGLPENAVNDLICPPCCAPLICALGDLGCFPTWVATVPTSTTPTFVFTGTCV
Avilll_Aac	TVKGLAVGIGSHWVLCIPTDGGNLLAVGDDGCFPTWVATVPTSTTPTFVFTGTCV
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GH74_Ace	DYASLNPSTTIVLACSFDPCCQPVDRIVAFCTDGGNLLAVGDDGCFPTWVATVACGCCR
Avilll_Aac	DYAGNKPNTIVRSCGADDPF-TIALCCNFCGCTWVADYACTSTPCTAVLACGCBT

GH74_Acc	PWAPCDPGDPPVPPVAVGFGNQWANACQCPVPAQGQIRGDRVNPKTFYALSNCTFYRSTDCCV
Avilll_Acc	VLLMGGTSGALVXGQQ
<hr/>	
GH74_Acc	TPQPVAAACLPSSCCAVGVMFHAVPCKSCDLWLAASSGLYHGTNGGGSWAL
Avilll_Acc	CPTKTVG LGGCTTVNATR AHPSTACDVAESTDKLWHSTDVCSTPPQICSGGTTAGWCF
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GH74_Acc	CPCKSAAPC88VAVVWVQGCGVGAATRCDDCCTTWWLLENDQEVCN WGGATTGDKHAN
Avilll_Acc	CPCKSAAPC88VAVVCPFTDCAGVNLWVQGCGVGAATRCDDCCTTWWLLENDQEVCN WGGATTGDKHAN
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GH74_Acc	LRRPVFGTNGRGRVPPRIGEPRPQ
Avilll_Acc	VGRVPRGHTPGRHGRGGRSPQ
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2. (Previously Presented) The composition of claim 1 wherein the Avilll peptide is further defined as comprising a linker and a signal sequence.

3. (Cancelled)

4. (Previously Presented) The composition of claim 1 or 2 wherein the carbohydrate binding domain (CBD) III of the Avilll peptide is further defined as comprising a length of about 80 to about 150 amino acids.

5. (Previously Presented) The composition of claim 1 or 2 wherein the carbohydrate binding domain (CBD) III of the Avilll peptide is further defined as comprising a length of about 90 amino acids.

6. (Previously Presented) The composition of claim 1 wherein the glycosyl hydrolase family 74 enzyme catalytic domain is further defined as including a polypeptide sequence identical to SEQ ID NO: 3.

7. (Previously Presented) The composition of claim 1 wherein the carbohydrate binding domain (CBD) III is further defined as comprising the polypeptide sequence of SEQ ID NO: 4.

8. (Previously Presented) The composition of claim 1 wherein the carbohydrate-binding domain (CBD) III is further defined as comprising the polypeptide sequence of SEQ ID NO: 5.

9. (Previously Presented) The composition of claim 1 wherein said Avilll protein comprises sequences identical to the polypeptides of SEQ ID NO: 3 and SEQ ID NO: 4.

10. (Previously Presented) The composition of claim 1, wherein the catalytic domain of GH74\_Ace has at least 90% sequence identity with SEQ ID NO: 3.

11. (Previously Presented) The composition of claim 1, wherein the catalytic domain of GH74 has at least 80% sequence identity with SEQ ID NO: 3.

12. (Previously Presented) An isolated Avill peptide having a polypeptide sequence of SEQ ID NO: 1.

13. (Cancelled)

14. (Previously Presented) An industrial mixture suitable for degrading cellulose, such mixture comprising the Avill polypeptide of claim 1.

15. (Currently Amended) The industrial mixture of claim 14 further defined as comprising a detergent.[]

16-27 (Cancelled)

28. (Previously Presented) An isolated polypeptide molecule comprising at least one polypeptide sequence selected from the group consisting of:

- a) a polypeptide sequence of SEQ ID NO: 3;
- b) a polypeptide sequence of SEQ ID NO: 4;
- c) a polypeptide sequence of SEQ ID NO: 5;
- d) a polypeptide sequence of SEQ ID NO: 1; and
- e) combinations thereof.

29. (Cancelled)

30. (Original) A fusion protein comprising the polypeptide of claim 28 and a heterologous peptide.

31. (Original) The fusion protein of claim 30, wherein the heterologous peptide is a substrate targeting moiety.

32. (Original) The fusion protein of claim 30, wherein the heterologous peptide is a peptide tag.

33. (Previously Presented) The fusion protein of claim 32, wherein the peptide tag is 6-His, thioredoxin, hemagglutinin, glutathione S-transferase, or OmpA signal sequence tag.

34. (Original) The fusion protein of claim 30, wherein the heterologous peptide is an agent that promotes polypeptide oligomerization.

35. (Original) The fusion protein of claim 34, wherein the agent is a leucine zipper.

36. (Original) A cellulase-substrate complex comprising the isolated polypeptide molecule of claim 28 bound to cellulose.

37-42 (Cancelled)

43. (Original) A composition comprising the polypeptide molecule of claim 28 and a carrier.

44-46. (Cancelled)

47. (New) The composition of claim 1 wherein said catalytic domain GH74\_Ace having a sequence identical to SEQ ID NO. 3 in each conserved position marked by an asterisk (\*), as shown below in comparison to *Aspergillus aculeatus* Avicelase III (AvIII\_Aac):

GH74\_Ace ATTQPYTWSNVIAGGGG-FVDGIVFNEGAPGILYVRTDIGGMYRWDAAANGRWIPLLDDWVG  
AvIII\_Aac AASQAYTWNVNTGGGGFTPQIVFVNPSAKGVAYARTDIGGAYRLNSDD-TWIPPLMDWVG

GH74\_Ace WNNWGYGVVSIADPINTNKWMAAVGMYTNWDPMGDAILRSESDQGATWQITPLPFKLG  
AvIII\_Aac NDTWHDWGIDALATDPVTDTRVYAVGMYTNEWDPMVGSILRSTDQGDTWETKLPFVKVG

GH74\_Ace GNMPGRGMGERLAQDPNNNDNLLYFGAPSGKGLWRSTDGSQATWSQMTNFPDVGTYLANPTD  
AVIII\_Aac GNMPGRGMGERLAQDPNNNSLLYFGARSQGHGLWKSTDYGATWSNVTSPTWGTYFQDSSS

**GH74\_Ace** TTGYQSDIQGVVVVAFDKSSSSLGQASKTIPFGVADPNNPVFWSRDGGATWQAVPGAP-TT  
**AvIII\_Aac** -T-YTSDFVGIANVTPDSTSGSSGSATPRIFGVADAGKSVPKSEDAGATWAWVSGEPQY

**GH74\_Ace** GFIPIHKGVFDPVNVHLYIATSNTPGYPDGGSSGDVWKFSVTSGTWRISFVPSTDTANDYF  
**AVI777\_Aac** GFLPHKGVLSPSEEKTLYISYANGAGPYDGTGNTVHKYNTSGVWTDISP---TSLASTYY

GH74_Ace	GYSGLTIDRQNPNTIMVATQISWWPDITIIPRSTDGGATWTRIWDTSYPNRSLRYVLDIS
AviIII_Aac	GYGGLSVDLQVPGTLMAVAALNCWWPDELIFRSTDGATWSPIWENNGYPSINYYSYDIS ***:***:***:***:***:***:***:***:***:***:***:***:***:***:***
GH74_Ace	AEPWLTFGVQPNPPVPSPKLGMDEAMAIDPFNSDRMLYGTGATLYATNDLTWDSCGGQI
AviIII_Aac	NAPWQDTTSTDQFP--VRVGWMVLAIDPFDSNHLYGIGLTIVYGGHDLITWDSCGGQI ***:***:***:***:***:***:***:***:***:***:***:***:***:***:***
GH74_Ace	HIAPMVKGLEETAVNDLISPPSGAPLISALGDLGGFTADVTAVPSTIFTSPVPTTGTSV
AviIII_Aac	TVKSLAVGIEEMAVLGLITPPCGPALLSAVGDDCGFYHSDLAAAPNQAYHTPTYGTTINGI ***:***:***:***:***:***:***:***:***:***:***:***:***:***:***
GH74_Ace	DYAEILNPPIIIVRAGSFDPSQPNDRHVAFSTDGGKKNWFQGSEPGGVITGGTVAA\$ADGSR
AviIII_Aac	DYAGNPKPSNIVRSGASDDYP----TLALSSNPGSTWYADYAASTSTGTIAVALSADGDT ***:***:***:***:***:***:***:***:***:***:***:***:***:***:***
GH74_Ace	FVWAPGDPGQPVVYAVGFGNSWAASQGVPNANAQIRSDRKVNPKTFYALSGNTFYRSTDGGV
AviIII_Aac	VLLMSSTSGALVSKSQG---TITA VSSLPSGAVIAGDKSDNTVFPYGGSAGAIYVSKDTAT ***:***:***:***:***:***:***:***:***:***:***:***:***:***:***
GH74_Ace	TFQFVAAGLPSSGAVGVMFHAVPGKEGDLWLAAASSGLYHSTNGGSSWSAI-TGVSSAVNV
AviIII_Aac	SFTKTIVS-LGSSTTIVNAIR-AHPSIAGDVWASTDKGLWHSTDYGSTPTQIGSGVTAGWSF ***:***:***:***:***:***:***:***:***:***:***:***:***:***:***
GH74_Ace	GFGKSAPGSSYPAVFWVGTIGGVITGAYRSDDCGTTWVLINDDQHQYGN-WGQAITGDHAN
AviIII_Aac	GFGKASSTGSYVVIYGFTIDGAAGLFKSEDAGTNWQVISDASHGFGSGSANVUNGDLQT ***:***:***:***:***:***:***:***:***:***:***:***:***:***:***
GH74_Ace	LRRVYIGTNGRGIVYGDIGGAPSG
AviIII_Aac	YGRVFRGHERPGHLLRQSQRREPAG ***:***:***:***:***:***

48. (New) The composition of claim 47 wherein said AviIII peptide retains at least the same level of cellulase activity and thermal tolerability as those exhibited by the peptide of SEQ ID NO. 1.

49. (New) A composition comprising a substantially purified AviIII peptide having at least 99% identity to SEQ ID NO. 1, said AviIII peptide comprising a catalytic domain of a glycosyl hydrolase family 74 (GH74\_Ace) enzyme and a carbohydrate binding domain (CBD) III.

50. (New) The composition of claim 49 wherein said catalytic domain GH74\_Ace having a sequence identical to SEQ ID NO. 3 in each conserved position marked by an asterisk (\*), as shown below in comparison to *Aspergillus aculeatus* Avicelase III (AviIII\_Aac):

GH74_Ace	ATTQPYTWSNVAIGGGG-FVDGIVFNEGAPGILYVVRTDIGGMYRWDAAANGRWIPLLDWVG
AviIII_Aac	AASQAYTWWKVVVTGGGGFTPGIVFNPNSAKGVAYARTDYGAYRLNSDD-TWTPPLMDWVG ***:***:***:***:***:***:***:***:***:***:***:***:***:***:***:***
GH74_Ace	WNNWGYNGVVSIAADPINTNKVVAAGMYTNWDPNDGAILRSSDQGATWQITPLPPKLG
AviIII_Aac	NDTWHDWGIDALATDPVDTDRVYVAVGMYTNEWDPNVGSIILRSTDQGDTWETKLPFKVG ***:***:***:***:***:***:***:***:***:***:***:***:***:***:***:***
GH74_Ace	GNMPGRGMGERLAVDPNNNDNLYFGAPSGKGLWRSTDGATWSQMTNFPDVGTYIANPTD
AviIII_Aac	GNMPGRGMGERLAVDPNKN\$ILYFGARSGHGLWKSTDYGATW\$NVT\$FTWTGTYFQDSSS *****:*****:*****:*****:*****:*****:*****:*****:*****:*****:*****:*****

GH74_Ace	TTGYQSDIQGVVVVAFDKSSSSLGQASKTIFVGVADPNNPVPWSRDGGATWQAVPGAP-T
AviIII_Aac	T--YT\$DPVGIAWVTFDST9GSSGSATPRIFVGVADAGKSVFKSEDAGATWAWVSGBPQY * * * * * ; * ; * ; * ; * ; * ; * ; * ; * ; * ; * ; * ; * ; * ; * ; * ; * ;
GH74_Ace	GFIPHKGVPDPVNMLVLYIATSNIGGYDGSQGDVWKPSVTSGTWTRISPVPSSTDNTANDYF
AviIII_Aac	GFLPHKGVLSPPEKTLIYISVANGAGPYDGTNGTVHKNITSGVMTDISP---TSLASTYY * * ; * * * ; * ; * ; * ; * ; * ; * ; * ; * ; * ; * ; * ; * ; * ; * ;
GH74_Ace	GYSGLTIDROHPNTIMVATQISWNPDIIIFRSTDGGATWTRIWDWTSPNRSIRYVLDIS
AviIII_Aac	GYGGLSVDLQVPGTLMVAALNCWNPDELIIFRSTDGGATWSPIEWNGPSINYYYSYDIS * * ; * * ; * ; * ; * ; * ; * ; * ; * ; * ; * ; * ; * ; * ; * ; * ;
GH74_Ace	AEPWLTFGVQPNNPPVPSPKLGWMDEAMAIDPPNSDRMLYGTGATLYATNDLTWDSDGGQI
AviIII_Aac	NAPWIQDTTSTDQFP---VRVGWMVEAALIDPFDSHMLYGTGLTVYGGHDLTNWDSIGHNV * * ; * * ; * ; * ; * ; * ; * ; * ; * ; * ; * ; * ; * ; * ; * ;
GH74_Ace	HIAPMVKGLEETAVNDLISPPSCAPLISALGDLGGFTHADVTAVPSTIFTSPVFTTGTSV
AviIII_Aac	TVKSLAVGIEEMAVILGLITPPGGPALLSAVGDDGGFYHSDLDAAPNQAYHTPTYGTINIG * * ; * * ; * ; * ; * ; * ; * ; * ; * ; * ; * ; * ; * ; * ; * ;
GH74_Ace	DYAEILNPSSIVRAGSFDPSSQPNDRHVAFSTDGGKRNWFQGSEPGGVITCGTVAAASADGSR
AviIII_Aac	DYAGNKPSSIVRSGASDDYP---TLALSSNFGSTWYADYAASTSTGTGAVALSADGDT * * ; * * ; * ; * ; * ; * ; * ; * ; * ; * ; * ; * ; * ; * ;
GH74_Ace	FVWAPGDPGOPVYAVGFGNSWAASQGV PANQIRSDRVNPKTFYALSGNTPYRSTDGGV
AviIII_Aac	VJLMSSSTS GALVSKSQG---TLTAVSSLPSGAVIASDKSDNTVYGGSAGAIYVSKNTAT * * ; * * ; * ; * ; * ; * ; * ; * ; * ; * ; * ; * ; * ;
GH74_Ace	TFQFWAAGLPSGAVGVMPHAvgKEDLWLAASSGLYHSTNGSSWSAI-TGVSSAVNV
AviIII_Aac	SPTKTWS-LGSSTTVNAIR-AHPSIAGDVWASTDKGLWHSTDYGSTFTQIGSGVTAGNSF * * ; * * ; * ; * ; * ; * ; * ; * ; * ; * ; * ; * ; * ;
GH74_Ace	GFGKSAAPGSSYPAVFVUGTIGGVIGAYRSDDCGTTWVLINDDQHQYGN-WGQAITGDHAN
AviIII_Aac	GPGKASSTGSSVVIYGGFTIDGAACLFKSEDAGTNWQVISDASHGFGSGSANVNGDLQT * * ; * * ; * ; * ; * ; * ; * ; * ; * ; * ; * ; * ; * ;
GH74_Ace	LRRVYIGTNGRGLIVYGDIGGAPSG
AviIII_Aac	YGRVFRGHERPGHLLRQSREPAQ * * ; * ; * ; * ; * ;

51. (New) The composition of claim 50 wherein said AviIII peptide retains at least the same level of cellulase activity and thermal tolerability as those exhibited by the peptide of SEQ ID NO. 1.

52. (New) A composition comprising a substantially purified AviIII peptide having an amino acid sequence identical to SEQ ID NO. 1, said AviIII peptide comprising a catalytic domain of a glycosyl hydrolase family 74 (GH74\_Ace) enzyme and a carbohydrate binding domain (CBD) III.

53. (New) A composition comprising a substantially purified AviIII peptide, said AviIII peptide comprising a catalytic domain of a glycosyl hydrolase family 74 (GH74\_Ace) enzyme and a carbohydrate binding domain (CBD) III, said catalytic domain GH74\_Ace having a sequence that is at least 90% identical to SEQ ID NO. 3.

54. (New) The composition of claim 51 wherein said catalytic domain  
GH74\_Ace has a sequence identical to SEQ ID NO. 3.